

SEQUENCE PROTOCOL <110> Þegussa AG <120> New nucleotide sequences which code for the mikE17 gene <130> 00\0561 BT <140> <u> 1</u>0 <141> <160> 4 <170> PatentIn Ver. 2.1 15 <210> 1 <211> 1890 <212> DNA <213> Corynebacterium glutamicum 20 <220> <221> CDS <222> (252)..(1673) <223> mikE17 gene 25 <400> 1 aaccccgttt ggtatcaacc a\aaagttta gacagcccaa ccttccgatc cagggagcaa 60 ctttgcgcag gtgacacaat tat ccaaca gttgcaccgt aggtgcctaa aaagttcccg 120 30 gggcggatgt ggcccgacca cgcc $\phi$ ggcac ctggtggcgg cgggctgcgt cgaaaagcga 180 aaatcaacaa gtttgcaaca cctcagtgcc aagagtggtt aaggtgatgg tgatcacgct 240 35 atagttgcgc c atg gga aag aca  $t_{\!\!\!/}$ at gtg ggg tcc agg ctg cgc caa ctg Met Gly Lys Thr Tyr Val Gly Ser Arg Leu Arg Gln Leu cgc cgc gaa aga gac ctg agc cag gca tcc tta gca gca acc ctt ggc 338 40 Arg Arg Glu Arg Asp Leu Ser Gln Ala Ser Leu Ala Ala Thr Leu Gly tta tot goa agt tat gta aat cag att  $\$ gag cac gac gta cgc ccg otc 386 Leu Ser Ala Ser Tyr Val Asn Gln Ile 🔃 His Asp Val Arg Pro Leu 45 30 acc gta ccg gtg tta ttg cgc atc acc gag gcg ttc ggc gta gac gca Thr Val Pro Val Leu Leu Arg Ile Thr Glu Ala Phe Gly Val Asp Ala 434 55 50 acg ttt ttc tcc cgc gac gat gac tcc cgc  $c \nmid g$  ctc gcc gag gtc caa 482 Thr Phe Phe Ser Arg Asp Asp Asp Ser Arg Let Leu Ala Glu Val Gln 55 gac gtc atg ctg gac cgg gag atc aat cct gcg aac gtg gag ctg caa Asp Val Met Leu Asp Arg Glu Ile Asn Pro Ala Asn Val Glu Leu Gln 530 90 80 85

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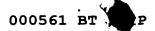
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